

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 27, 2005, 20:54:04 ; Search time 126 Seconds
(without alignments)
11058.472 Million cell updates/sec

Title: US-10-038-854-38

Sequence: 14495
1 MDVKERRPYCSLTLSRRERK.....ELADSNANIQPLROSEIGRR 2721

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt_03.*
1: uniProt_sprot.*
2: uniProt_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14248	98.3	2715	2 Q9WTS6	Q9WTS6 mus musculus
2	12351	85.2	2346	2 Q9JLC1	Q9JLC1 mus musculus
3	11627	80.2	2590	2 Q9W7R4	Q9W7R4 brachydanio
4	10403	71.8	2765	2 Q9RIK2	Q9RIK2 rattus norv
5	10393.5	71.7	2802	2 Q9DERS	Q9DERS gallus gall
6	10393.5	71.7	2764	2 Q9WTS5	Q9WTS5 mus musculus
7	10189	70.3	2771	2 Q9WTS7	Q9WTS7 mus musculus
8	9764.5	69.0	2825	2 Q70465	Q70465 mus musculus
9	9764.5	67.4	2824	2 Q9W7R3	Q9W7R3 brachydanio
10	9489	65.5	1828	2 Q80TJ2	Q80TJ2 mus musculus
11	9267	63.9	1769	2 Q9W6T6	Q9W6T6 homo sapien
12	9035	62.3	2705	2 Q9W6T6	Q9W6T6 gallus gall
13	8972	61.9	2731	2 Q9WTS4	Q9WTS4 mus musculus
14	8884	61.3	2725	2 Q9UKZ4	Q9UKZ4 homo sapien
15	8463.5	58.4	2144	2 Q9ULU2	Q9ULU2 homo sapien
16	8368	57.7	2192	2 Q804R1	Q804R1 brachydanio
17	5447	37.6	1045	2 Q9NW11	Q9NW11 homo sapien
18	5313	36.7	1399	2 Q6N022	Q6N022 homo sapien
19	5040	34.8	964	2 Q9NV77	Q9NV77 mus musculus
20	4470.5	30.8	1198	2 Q80TF5	Q80TF5 mus musculus
21	4061.5	28.0	1086	2 Q9P2P4	Q9P2P4 homo sapien
22	4037.5	27.9	1071	2 Q7Z3C7	Q7Z3C7 homo sapien
23	3930.5	27.1	2633	2 Q7OKI2	Q7OKI2 anopheles g
24	3847	26.5	2731	2 Q6I307	Q6I307 drosophila
25	3847	26.5	2731	2 Q9VNU6	Q9VNU6 drosophila
26	3839	26.5	2515	2 Q24551	Q24551 drosophila
27	3839	26.5	2731	2 Q18366	Q18366 drosophila
28	3571.5	24.6	3004	2 Q24550	Q24550 drosophila
29	3569.5	24.6	3004	2 Q9VYH8	Q9VYH8 drosophila
30	3520.5	24.3	2754	2 Q7PRV4	Q7PRV4 anopheles g
31	3489.5	24.1	930	2 Q9JLCO	Q9JLCO mus musculus

32	3416	23.6	991	2 Q8CAT1	Q8CAT1 mus musculus
33	3283	22.6	625	2 Q96SY2	Q96SY2 homo sapien
34	3213.5	22.2	849	2 Q9WTS6	Q9WTS6 homo sapien
35	2809	19.4	730	2 Q9WTS6	Q9WTS6 homo sapien
36	2784	19.2	831	2 Q9PU49	Q9PU49 gallus gall
37	2316	16.0	442	2 Q9NZJ2	Q9NZJ2 homo sapien
38	2237	15.4	2560	2 Q21980	Q21980 caenorhabdi
39	2198.5	15.2	2531	2 Q8WP22	Q8WP22 caenorhabdi
40	1673.5	11.5	329	2 Q8BSL5	Q8BSL5 mus musculus
41	1531	10.6	337	2 Q9RIK0	Q9RIK0 rattus norv
42	1178.5	8.1	272	2 Q9RIJ9	Q9RIJ9 rattus norv
43	1155.5	8.0	266	2 Q9RIK1	Q9RIK1 rattus norv
44	1154	8.0	229	2 Q9QY21	Q9QY21 mus musculus
45	1096	7.6	536	2 Q8C8D2	Q8C8D2 mus musculus

ALIGNMENTS

RESULT 1	ID	Q9WTS6	PRELIMINARY;	PRT;	2715 AA.
AC	Q9WTS6	Q9WTS6			
DT	01-NOV-1999	(TEMBLrel. 12, Created)			
DT	01-NOV-1999	(TEMBLrel. 12, Last sequence update)			
DT	01-MAR-2004	(TEMBLrel. 26, Last annotation update)			
DE	Ten-m3.				
GN	Name=Od23; Synonyms=ten-m3;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
FM	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Balb/c; TISSUE=Brain;				
RA	Ochoaehi T., Zhou X., Peng K., Richter B., Moergelin M., Perez M.T.,				
RA	Su W., Chiquet-Ehrismann R., Rauch U., Passler R.,				
RT	"Mouse Ten-m/Od23 is a new family of dimeric type II transmembrane				
RT	proteins expressed in many tissues."				
RL	J. Cell Biol. 0:0-0(1999).				
CC	-1- SIMILARITY: Contains 8 EGF-like domains.				
DR	EMBL; AB025412; BAA7398.1; --				
DR	HSP; P00750; ITPG.				
DR	KGD; MGI:1345183; Od23.				
DR	InterPro; IPR011044; Amino_DH_B_1like.				
DR	InterPro; IPR000742; EGF_2.				
DR	InterPro; IPR006209; EGF_1like.				
DR	InterPro; IPR006210; IEGF.				
DR	InterPro; IPR001258; NHL.				
DR	InterPro; IPR009041; FMP_SGCI.				
DR	InterPro; IPR009471; Ten_N.				
DR	InterPro; IPR006530; YD.				
DR	Pfam; PF00006; EGF_3.				
DR	Pfam; PF01436; NHL_6.				
DR	Pfam; PF05593; RKS_repeat; 6.				
DR	Pfam; PF06484; Ten_N_1.				
DR	SMART; SM00181; EGF_7.				
DR	TIGRFAMs; TIGR01643; YD_repeat_2x; 5.				
DR	PROSITE; PS00023; EGF_1; 8.				
DR	PROSITE; PS01186; EGF_2; 7.				
DR	PROSITE; PS50026; EGF_3; 3.				
KW	EGF-like domain.				
SQ	SEQUENCE 2715 AA; 303063 MW; 598F46A7734C2B1 CRC64;				
Query Match	98.3%;	Score 14248;	DB 2;	Length 2715;	
Best Local Similarity	97.9%;	Pred. No. 0;			
Matches 2664;	Conservative 33;	Mismatches 18;	Indels 6;	Gaps 1;	
QY	1 MDVKERRPYCSLTLSRRERKRYTNSADNBEGRVPTQKSYSSSELTAKAFDHSRLLYG 60				
DB	1 MDVKERRPYCSLTLSRRERKRYTNSADNBEGRVPTQKSYSSSELTAKAFDHSRLLYG 60				
QY	61 NRYVDLVHREADFTQOGNFTLRQLGVCPEATRRGLAFCAMWGLPHRGYSISAGSDADT 120				

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OM protein - protein search, using sw model

Run on: September 27, 2005, 20:56:29 ; Search time 32 Seconds
(without alignments)
8181.432 Million cell updates/sec

Title: US-10-038-854-38

Perfect score: 1495
Sequence: 1 MDVRRPYSCTLRKREKE.....ELADSNNTQFLRQSEIGRR 2721

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR 79.*

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	10001	69.0	2825 2	T14271 Doc4 protein, stre
2	3839	26.5	2515 2	S47008 tenascin-like prot
3	3534	24.4	2406 2	AS4148 odz protein - fru
4	3213.5	22.2	849 2	T46253 hypothetical prote
5	2226.5	15.4	2531 2	T16743 hypothetical prote
6	1184.5	8.2	782 2	A61625 tenascin-like prot
7	703	4.8	2019 1	J01322 tenascin precursor
8	699	4.8	2201 2	A32150 tenascin-C - human
9	689	4.8	184 2	T12457 hypothetical prote
10	680.5	4.7	1746 1	S19694 tenascin precursor
11	659.5	4.5	1810 1	A32630 tenascin precursor
12	637	4.4	4006 2	T09070 probable tenascin
13	616	4.2	3566 1	A40701 tenascin-X - precu
14	590	4.1	4135 2	T42629 tenascin-X - bovin
15	589	4.1	647 2	A43902 tenascin - eastern
16	472.5	3.3	1620 2	T27283 hypothetical prote
17	455.5	3.1	1203 2	A49175 Notch B protein -
18	455.5	3.1	2471 2	A49128 cell-fate determin
19	448.5	3.1	3191 2	T22945 hypothetical prote
20	427.5	2.9	2703 1	A24420 notch protein - fr
21	424.5	2.9	2555 2	A40043 notch protein homo
22	421.5	2.9	2531 1	JH0675 restrictin precurs
23	419	2.9	1533 2	S18188 notch protein homo
24	419	2.9	2531 2	A46019 fibronectin Ia - s
25	417.5	2.9	1064 2	A40136 hypothetical prote
26	417.5	2.9	1111 2	T26972 jagged protein pre
27	417.5	2.9	1220 2	S78549 notch protein - h
28	417.5	2.9	2321 2	S78549 notch protein - h
29	416.5	2.9	2318 2	S45306

30	414.5	2.9	1356 2	A45445 janusin precursor,
31	413.5	2.9	1574 2	T13954 MEGR protein - ra
32	402.5	2.8	2437 2	S42612 transmembrane prot
33	402.5	2.8	2524 2	A35844 Notch protein - Af
34	389.5	2.7	473 2	A56175 adhesive plaque pr
35	388.5	2.7	1964 2	T09059 notch4 - mouse
36	388	2.7	1408 2	S16148 gene seerate prote
37	385.5	2.7	2139 2	A35672 crumb protein - f
38	384.5	2.7	1732 2	E89753 protein Flt7.4 (1
39	384	2.6	2531 2	T31070 notch homolog - be
40	382	2.6	2352 2	T30201 Notch homolog prot
41	377.5	2.6	1295 2	A32901 glp1 protein precu
42	370	2.6	2334 2	S32920 cell wall associat
43	365	2.5	1429 2	S06434 homeotic protein 1
44	360.5	2.5	832 2	A31246 neurogenic protein
45	360.5	2.5	880 2	S00670 neurogenic repetit

ALIGNMENTS

RESULT 1
T14271
Doc4 protein, stress-induced - mouse
N/Alternate names: odz protein homolog
C/Species: Mus musculus (house mouse)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T14271
R/Mang, X.Z.; Kuroda, M.; Sok, J.; Batchvarova, N.; Kimmel, R.; Chung, P.; Zluzner, H.
EMBL J. 17 3619-3630, 1998
A/Title: Identification of novel stress-induced genes downstream of chop.
A/Reference number: Z17951; MUID:98315054; PMID:9649432
A/Accession: T14271
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-2825 <MAN>
A/Cross-references: UNIPROT:O70465; EMBL:AF059485; NID:g3170614; PID:g3170615; PIDN:AAC
A/Genetics:
A/Gene: Doc4

QY	Query Match	69.0%	Score 10001;	DB 2;	Length 2825;
DB	Best Local Similarity	64.6%	Best. No. 0;		
	Matches 1850;	Conservative 364;	Mismatches 469;	Indels 180;	Gaps 23;
QY	1	MDVRRPYSCTLRKREKERYTNSADNBECPYOKSYSSSEITAKADHDSRLLYG	60		
DB	1	MDVRRPYSCTLRKREKERYTNSADNBECPYOKSYSSSEITAKADHDSRLLYG	57		
QY	61	NRVADLVHRADEPFTQGNFTLRQLGVCCEPATRRGLAFCAMGLPHRGYSISASDADT	120		
DB	58	SRVADWVPGAEFEFCRTGTFTRLELGLGEMTPPHGLTYRTDGLPHCGYSMGASDADL	117		
QY	121	ENRANVSPHMANLNGRGVSGSSCLSSRSNALTITDREHN	164		
DB	118	EADTVASPEHPVRLMGSTRSGSSCLSSRSNALTITDREHN	177		
QY	165	-----KSDSR-----	NEOP 173		
DB	178	IEGSPSPSPPNBESORLLGNGVAPTPDSDSEEFVNSPLVKSASLGVAAANDHP	237		
QY	174	ASNQGGSTIQ-----PLPPSHKQSAOH-PSITSLNNSLTJNRNOSPAP-----PA	220		
DB	238	SSIQNHRLRTPPPLPHATPPN-QHHAASINSLNKGNFTPRSNBPAPADHSLSGEP	295		
QY	221	ALPAELQTPRESVQLQDSWTLGNNVPLESR-----	250		
DB	296	AGSAQ-----EPHAQDNWVNLNSKIPETNLKQPLFTGWQNDLLEMDIFASRRDGAY	350		
QY	251	---HFLPKTGTGTTPFSTATPGYTMAAGSVSPPTPLPRNTLSASAFKSKSKYCSW	307		
DB	351	SDGHFFPKKG-GTSPLFCITSPGYPLTSSVYVPPPRPLPRSFSPAPVLLKKPSKCNW	409		
QY	308	KCTALCAVGSVLAAILLSYFIAMHLFGLNMWLOQTEMDTTFENGKVNSDT-----MPTNT	362		

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OM protein - protein search, using sw model

Run on: September 27, 2005, 21:02:29 ; Search time 114 Seconds
(without alignments)
9715.053 Million cell updates/sec

Title: US-10-038-854-38

Perfect score: 14495
1 MDVKEKRRPYCSLTYSRRERE.....ELADSNNTQFLROSEIGRR 2721

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1826554 seqs, 407025358 residues

Total number of hits satisfying chosen parameters: 1826554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PCRTUS_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppaa/PCRTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubppaa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubppaa/US10F_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubppaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14495	100.0	2721	US-10-038-854-38	Sequence 38, Appl
2	14475	99.9	2725	US-10-038-854-36	Sequence 36, Appl
3	14248	98.3	2715	US-10-042-865-52	Sequence 52, Appl
4	14248	98.3	2715	US-10-029-020-51	Sequence 51, Appl
5	13944.5	96.2	2628	US-10-038-854-40	Sequence 40, Appl
6	13834	95.4	2613	US-10-038-854-42	Sequence 42, Appl
7	12351	85.2	2346	US-10-072-012-491	Sequence 491, Appl
8	11627	80.2	2590	US-10-072-012-490	Sequence 490, Appl
9	10403	71.8	2765	US-09-808-602-84	Sequence 84, Appl
10	10403	71.8	2765	US-09-800-198-72	Sequence 72, Appl
11	10403	71.8	2765	US-10-072-012-488	Sequence 488, Appl

12	10394.5	71.7	2802	US-09-808-602-81	Sequence 81, Appl
13	10394.5	71.7	2802	US-09-800-198-69	Sequence 69, Appl
14	10394.5	71.7	2802	US-10-072-012-489	Sequence 489, Appl
15	10394	71.7	2759	US-10-072-012-144	Sequence 144, Appl
16	10393.5	71.7	2764	US-09-808-602-80	Sequence 80, Appl
17	10393.5	71.7	2764	US-09-800-198-68	Sequence 68, Appl
18	10393.5	71.7	2764	US-10-072-012-487	Sequence 487, Appl
19	10347.5	71.4	2794	US-10-042-865-13	Sequence 13, Appl
20	10310.5	71.1	2724	US-09-808-602-13	Sequence 13, Appl
21	10310.5	71.1	2724	US-09-800-198-13	Sequence 13, Appl
22	10309	71.1	2733	US-09-808-602-8	Sequence 8, Appl
23	10309	71.1	2733	US-09-800-198-8	Sequence 8, Appl
24	10221	70.5	2769	US-10-029-020-14	Sequence 14, Appl
25	10221	70.5	2769	US-10-029-020-14	Sequence 14, Appl
26	10189	70.3	2771	US-09-808-602-82	Sequence 82, Appl
27	10189	70.3	2771	US-09-808-602-82	Sequence 82, Appl
28	10144.5	70.0	2758	US-10-467-535-10	Sequence 10, Appl
29	10078	69.5	2633	US-10-144-194A-82	Sequence 82, Appl
30	10078	69.5	2633	US-10-491-566-82	Sequence 82, Appl
31	10010	69.1	2775	US-10-383-201-56	Sequence 56, Appl
32	9491	65.5	2551	US-10-144-194A-80	Sequence 80, Appl
33	9491	65.5	2551	US-10-491-566-80	Sequence 80, Appl
34	9267	63.9	1769	US-10-723-860-4494	Sequence 4494, Appl
35	8964	61.8	2725	US-10-029-020-52	Sequence 52, Appl
36	8964	61.8	2725	US-10-408-765A-1687	Sequence 1687, Appl
37	8884	61.3	2725	US-10-295-027-928	Sequence 928, Appl
38	8884	61.3	2725	US-10-723-860-4102	Sequence 4102, Appl
39	8463.5	58.4	2144	US-10-723-860-2303	Sequence 2303, Appl
40	6702.5	46.2	1737	US-09-808-602-83	Sequence 83, Appl
41	6702.5	46.2	1737	US-09-800-198-71	Sequence 71, Appl
42	6523.5	45.0	1688	US-10-144-194A-113	Sequence 113, Appl
43	6523.5	45.0	1688	US-10-491-566-113	Sequence 113, Appl
44	6523.5	45.0	1688	US-10-494-940-52	Sequence 52, Appl
45	5447	37.6	1045	US-10-042-865-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-10-038-854-38
Sequence 38, Application US/10038854
Publication No. US20040022781A1
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Li, Li
APPLICANT: Wolenc, Adam R
APPLICANT: Verne, Corine
APPLICANT: Eisen, Andrew J
APPLICANT: Liu, Xiaohong
APPLICANT: Malyankar, Uriel M
APPLICANT: Shinkets, Richard A
APPLICANT: Tchernev, Velizar
APPLICANT: Spaderna, Steven K
APPLICANT: Gorman, Linda
APPLICANT: Kektura, Ramesh
APPLICANT: Paturajan, Meera
APPLICANT: Gusev, Vladimir Y
APPLICANT: Gangoli, Beha A
APPLICANT: Guo, Xiaojia S
APPLICANT: Shenoy, Suresh G
APPLICANT: Rastelli, Luca
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Bugees, Catherine E
APPLICANT: Edinger, Shlomit R
APPLICANT: Eilerman, Karen
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glenda
APPLICANT: Millet, Isabelle
APPLICANT: MacDougall, John R
TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-230

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OM protein - protein search, using sw model

Run on: September 27, 2005, 20:57:04 ; Search time 32 Seconds
(without alignment)
6347.503 Million cell updates/sec

Title: US-10-038-854-38
Perfect score: 1495
Sequence: 1 MDVRRPYSITKSRREKE.....ELADSNINQFLRSEIGRR 2721

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1485	10.2	560	3 US-08-891-845-4	Sequence 4, Appli
2	1485	10.2	560	4 US-09-514-573-4	Sequence 4, Appli
3	1485	10.2	768	4 US-08-891-845-2	Sequence 2, Appli
4	1485	10.2	768	4 US-09-514-573-2	Sequence 2, Appli
5	839.5	5.8	501	3 US-08-891-845-10	Sequence 10, Appli
6	839.5	5.8	501	4 US-09-514-573-10	Sequence 10, Appli
7	639.5	4.8	2200	4 US-09-796-575-2	Sequence 2, Appli
8	687.5	4.7	2199	4 US-08-793-273C-2	Sequence 2, Appli
9	687.5	4.7	2199	5 PCT-US95-11684-2	Sequence 2, Appli
10	659.5	4.5	1810	4 US-08-793-273C-4	Sequence 4, Appli
11	659.5	4.5	1810	5 PCT-US95-11684-4	Sequence 4, Appli
12	615	4.2	2254	4 US-09-949-016-9270	Sequence 9270, Ap
13	446.5	3.1	2471	1 US-08-185-432-16	Sequence 16, Appli
14	446.5	3.1	2471	1 US-08-083-590A-19	Sequence 19, Appli
15	446.5	3.1	2471	3 US-08-533-384-19	Sequence 19, Appli
16	446.5	3.1	2471	4 US-08-899-232-1	Sequence 1, Appli
17	446.5	3.1	2471	4 US-09-121-457-1	Sequence 1, Appli
18	446.5	3.0	2703	1 US-08-185-432-19	Sequence 19, Appli
19	428.5	3.0	2703	4 US-08-899-232-4	Sequence 4, Appli
20	428.5	3.0	2703	4 US-09-121-457-4	Sequence 4, Appli
21	426	2.9	1193	2 US-08-400-159-10	Sequence 10, Appli
22	426	2.9	1193	3 US-08-611-729A-10	Sequence 10, Appli
23	426	2.9	1193	4 US-09-195-524-10	Sequence 10, Appli
24	418.5	2.9	1010	3 US-08-882-046-7	Sequence 7, Appli
25	418.5	2.9	1010	4 US-09-566-047-6	Sequence 6, Appli
26	418.5	2.9	1036	3 US-09-068-740A-6	Sequence 7, Appli
27	418.5	2.9	1067	4 US-09-579-536C-18	Sequence 18, Appli

28	418.5	2.9	1187	3 US-09-068-740A-7	Sequence 7, Appli
29	418.5	2.9	1208	4 US-09-199-865-1	Sequence 1, Appli
30	418.5	2.9	1208	4 US-10-213-329-1	Sequence 1, Appli
31	418.5	2.9	1218	2 US-08-400-159-6	Sequence 6, Appli
32	418.5	2.9	1218	3 US-08-611-729A-6	Sequence 6, Appli
33	418.5	2.9	1218	3 US-08-882-046-2	Sequence 2, Appli
34	418.5	2.9	1218	3 US-09-068-740A-11	Sequence 11, Appli
35	418.5	2.9	1218	4 US-09-566-047-2	Sequence 2, Appli
36	418.5	2.9	1218	4 US-09-917-254-85	Sequence 85, Appli
37	418.5	2.9	1218	4 US-09-195-524-6	Sequence 6, Appli
38	418.5	2.9	1218	4 US-09-579-536C-1	Sequence 1, Appli
39	418.5	2.9	1218	4 US-09-949-016-5902	Sequence 5902, Ap
40	418.5	2.9	1234	4 US-09-949-016-10297	Sequence 10297, A
41	417.5	2.9	1219	3 US-08-882-046-5	Sequence 5, Appli
42	417.5	2.9	1219	4 US-09-566-047-5	Sequence 5, Appli
43	417.5	2.9	2321	4 US-09-230-652-2	Sequence 2, Appli
44	415	2.9	1055	3 US-09-214-278-2	Sequence 2, Appli
45	415	2.9	1055	4 US-09-855-722-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-08-891-845-4
: Sequence 4, Application US/08891845
: Patent No. 6096873
:
: GENERAL INFORMATION:
: APPLICANT: Schaefer, Gabriele M.
: APPLICANT: Sliwowski, Mark
: TITLE OF INVENTION: Gamma-Herregulin
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESS: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Winpatin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/891, 845
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/021640
: FILING DATE: 07/12/96
: ATTORNEY/AGENT INFORMATION:
: NAME: Lee, Wendy M.
: REGISTRATION NUMBER: 40,378
: REFERENCE/DOCKET NUMBER: P1043
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1994
: TELEFAX: 415/952-9881
:
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 560 amino acids
: TYPE: Amino Acid
: TOPOLOGY: Linear
:
: US-08-891-845-4
:
: Query Match 10.2%; Score 1485; DB 3; Length 560;
: Best Local Similarity 54.1%; Pred. No. 1.5e-103;
: Matches 311; Conservative 62; Mismatches 124; Indels 78; Gaps 13;
:
: Cx 1 MDVRRPYSITKSRREKRRRTNNSGADNBECKVPTOKYSSSETLKARDHDSRLTYG 60
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
: Db 1 MDVRRPYSITLR-RDARRRYTTSSADSBEGKAP-QKSYSSSETLKAYDQD-ARLAYG 57
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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 22:17:44 / Search time 16507 Seconds
(without alignments)
19934.913 Million cell updates/sec

Title: US-10-038-854-37
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
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1: gb_est1:*
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3: gb_hlc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5051.2	58.4	5094	9	AY405420 Homo sapi
2	4850	56.1	5069	9	AY405421 Pan trogl
3	3765.8	43.6	5087	9	AY405422 Mus muscu
4	2727.2	31.5	6246	9	AY413475 Homo sapi
5	2350.6	27.2	5970	9	AY413476 Pan trogl
6	1455	16.8	2627	3	AK050784 Mus muscu
7	1269.6	14.7	3190	9	AY413477 Mus muscu
8	1262	14.6	2926	3	AK050784 Mus muscu
9	1222.8	14.1	3038	3	AK037897 Mus muscu
10	940.6	10.9	3760	3	AK031268 Mus muscu
11	806.6	9.3	883	6	CD628955 56079503H
12	803.4	9.3	811	1	AU119933 AU119933
13	801	9.3	826	6	CD628960 56079619H
14	796	9.2	843	1	AU124680 AU124680
15	783.8	9.1	812	1	AU13387 AU13387
16	780.8	9.0	809	1	AU119743 AU119743
17	776	9.0	776	6	CA777388 1P19C06.x
18	775	9.0	868	6	CA454304 AGENCOURT
19	772.8	8.9	865	7	CK775005 963813 MA
20	760	8.8	848	7	CK773227 961842 MA
21	747.2	8.6	795	6	CD628956 56079503J
22	738.4	8.5	798	6	CD628958 56079603H
23	727.2	8.4	798	6	BE740880 601593111
24	724.6	8.4	732	7	CN391504 170005315

25	714.6	8.3	894	5	BU151768
26	711.6	8.2	776	1	BE741784
27	707.2	8.2	757	1	AU126844
28	700.4	8.1	916	5	BO892798
29	698.8	8.1	818	6	CD807778
30	695.6	8.0	951	5	BU839812
31	689.9	8.0	909	4	BP980526
32	688	8.0	720	7	CN391496
33	686.4	7.9	712	7	CN391503
34	681.8	7.9	716	7	CN391499
35	675.8	7.8	792	2	BE898900
36	659.4	7.6	681	2	BE382393
37	656.4	7.6	702	4	BM670316
38	655.6	7.6	854	7	CF745232
39	652.6	7.5	834	5	BU610605
40	646	7.5	658	7	CN391493
41	645.2	7.5	770	2	BE898495
42	642.8	7.4	687	6	CA428646
43	641.4	7.4	819	5	BO443891
44	640	7.4	724	4	BG419748
45	633.4	7.3	641	7	CN391495

ALIGNMENTS

RESULT 1	AY405420	5094 bp	DNA	linear	GSS 12-DEC-2003
LOCUS	AY405420				
DEFINITION	Homo sapiens HCM2218 gene, VIRUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
ACCESSION	AY405420				
VERSION	AY405420.1	GI:39761394			
KEYWORDS	GENE				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.J., Adams, M.D. and Cargill, M., 1960-1963 (2003)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Clivello, D.R., Lu, F., Murphy, B., Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Submitted (15-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	Direct Submission				
FEATURES	Location/Qualifiers				
SOURCE	1..5094				
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	/mol_type="genomic DNA"				
	/db_xref="taxon:9606"				
	<1..5094				
	/locus_tag="HCM2218"				
ORIGIN					
Query Match	58.4%;	Score 5051.2;	DB 9;	Length 5094;	
Best Local Similarity	99.4%;	Pred. No. 0;			
Matches 5084;	Conservative	0;	Mismatches 10;	Indels 21;	Gaps 1;
2901	GTTCAGCTGATGTCGCAATGATGTCGCTCTCAACTTGTATTTGAACATCCCATTT	2960			
1	GTTCAGCTGATGTCGCAATGATGTCGCTCTCAACTTGTATTTGAACATCCCATTT	60			

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OM nucleic - nucleic search, using sw model

Run on: September 27, 2005, 05:59:11, Search time 3289 Seconds
(without alignments)
17574.597 Million cell updates/sec

Title: US-10-038-854-37

Perfect score: 8645
Sequence: 1 ttctgcctcgagccagaatt.....actgtatttaactta 8645

Scoring table: IDENTITY NUC
Gapop 10'-0, Gapext 1.0

Searched: 7400732 seqs, 334337571 residues

Total number of hits satisfying chosen parameters: 14801464

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/FCI_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTTIS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	8000.6	92.5	8473	17	US-10-038-854-39
4	7895.8	91.3	8487	17	US-10-038-854-41
5	5952.8	68.9	6810	20	US-10-723-860-8301
6	5305.8	61.4	5309	20	US-10-723-860-4493
7	3714.8	43.0	8575	18	US-10-072-012-143

8	3614	41.8	3614	17	US-10-172-118-1743	Sequence 1743, Ap
9	3614	41.8	3614	18	US-10-342-887-1743	Sequence 1743, Ap
10	3614	41.8	3614	21	US-10-848-755A-185	Sequence 185, Ap
11	3589.8	41.5	8438	17	US-10-042-865-1	Sequence 1, Appl
12	3566.6	41.3	8409	9	US-09-808-602-79	Sequence 79, Appl
13	3566.6	41.3	8409	9	US-09-800-198-67	Sequence 67, Appl
14	3545.6	41.0	8797	9	US-09-808-602-74	Sequence 74, Appl
15	3545.6	41.0	8797	9	US-09-808-602-77	Sequence 77, Appl
16	3545.6	41.0	8797	10	US-09-800-198-62	Sequence 62, Appl
17	3545.6	41.0	8797	10	US-09-800-198-65	Sequence 65, Appl
18	3518.4	40.7	8689	9	US-09-808-602-78	Sequence 78, Appl
19	3518.4	40.7	8689	10	US-09-800-198-66	Sequence 66, Appl
20	3502.2	40.5	8354	17	US-10-383-201-43	Sequence 43, Appl
21	3502.2	40.5	8354	18	US-10-029-020-13	Sequence 13, Appl
22	3482.2	40.3	9826	9	US-09-808-602-77	Sequence 7, Appl
23	3482.2	40.3	9826	10	US-09-800-198-7	Sequence 7, Appl
24	3466.4	40.1	9695	17	US-10-144-194A-81	Sequence 81, Appl
25	3466.4	40.1	9695	20	US-10-491-566-81	Sequence 81, Appl
26	3453.8	40.0	9729	9	US-09-808-602-12	Sequence 12, Appl
27	3453.8	40.0	9729	10	US-09-800-198-12	Sequence 12, Appl
28	3439.2	39.8	8645	22	US-10-467-535-22	Sequence 22, Appl
29	3264.8	37.8	9058	17	US-10-144-194A-79	Sequence 79, Appl
30	3264.8	37.8	9058	20	US-10-491-566-79	Sequence 79, Appl
31	3249.6	37.6	8355	17	US-10-383-201-55	Sequence 55, Appl
32	3158	36.5	7781	20	US-10-723-860-2302	Sequence 2302, Ap
33	2854.8	33.0	8297	20	US-10-723-860-4101	Sequence 4101, Ap
34	2854.8	33.0	12880	17	US-10-295-027-927	Sequence 927, Ap
35	2670	30.9	6771	20	US-10-723-860-6509	Sequence 6509, Ap
36	2599	30.1	6560	9	US-09-808-602-76	Sequence 76, Appl
37	1671.2	19.3	8624	20	US-10-723-860-3169	Sequence 3169, Ap
38	1671.2	19.3	8624	22	US-10-756-149-2959	Sequence 2959, Ap
39	1615.2	18.7	8774	20	US-10-723-860-7116	Sequence 7176, Ap
40	1580.6	18.3	4245	21	US-10-494-940-38	Sequence 74, Appl
41	1580.6	18.3	4245	20	US-10-128-558-121	Sequence 121, Appl
42	1442	16.7	13217	14	US-10-198-846-13976	Sequence 13976, A
43	912.8	10.6	791	9	US-09-823-245A-85	Sequence 85, Appl
44	766.4	8.9	2496	9	US-09-808-602-75	Sequence 75, Appl
45	706	8.2				

ALIGNMENTS

RESULT 1
US-10-038-854-37
: Sequence 37, Application US/10038854
: Publication No. US20040022781A1
GENERAL INFORMATION: Kimberly A
APPLICANT: Spytek, Kimberly A
: APPLICANT: Li, Li
: APPLICANT: Wolenc, Adam R
: APPLICANT: Vernet, Corine
: APPLICANT: Eissen, Andrew J
: APPLICANT: Liu, Xiaohong
: APPLICANT: Malyanhar, Uriel M
: APPLICANT: Shimkets, Richard A
: APPLICANT: Tchervet, Velizar
: APPLICANT: Spaderna, Steven K
: APPLICANT: Gorman, Linda
: APPLICANT: Kekuda, Ramesh
: APPLICANT: Paturajan, Meera
: APPLICANT: Gueev, Vladimir Y
: APPLICANT: Gangolli, Esna A
: APPLICANT: Guo, Xiaojia S
: APPLICANT: Shenoy, Suresh G
: APPLICANT: Rastelli, Luca
: APPLICANT: Caeman, Stacie J
: APPLICANT: Boldog, Ferenc
: APPLICANT: Burgees, Catherine E
: APPLICANT: Edinger, Shlomit R
: APPLICANT: Killeman, Karen
: APPLICANT: Gunther, Erik
: APPLICANT: Smithson, Glenda

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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 22:25:30 / Search time 892 Seconds
(without alignments)
15858.310 Million cell updates/sec

Title: US-10-038-854-37

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued, Patents, NA: *
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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCUTS.COMB.seq: *
6: /cgn2_6/ptodata/1/ina/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	345.8	4.0	3111	US-09-514-573-1	Sequence 1, Appl
4	345.4	4.0	1680	US-08-891-845-3	Sequence 3, Appl
5	345.4	4.0	1680	US-09-514-573-3	Sequence 3, Appl
6	267.8	3.1	2387	US-08-891-845-11	Sequence 11, Appl
7	267.8	3.1	2387	US-09-514-573-11	Sequence 11, Appl
8	112.4	1.3	288	US-09-513-999C-23277	Sequence 23277, A
9	74.6	0.9	6049	US-08-793-273C-3	Sequence 3, Appl
10	74.6	0.9	6049	PCT-US95-11684-3	Sequence 3, Appl
11	72.2	0.8	3033	US-09-724-797-81	Sequence 81, Appl
12	70	0.8	1515	US-09-902-540-9184	Sequence 9184, Ap
C 13	70	0.8	9556	US-09-902-540-982	Sequence 982, App
14	69.6	0.8	28509	US-09-902-540-1240	Sequence 1240, Ap
15	68.6	0.8	6763	US-09-949-016-3399	Sequence 3399, Ap
16	68.6	0.8	13857	US-09-620-312D-75	Sequence 75, Appl
17	68.6	0.8	34534	US-09-949-016-15141	Sequence 15141, A
18	68.4	0.8	2244	US-09-902-540-9009	Sequence 9009, Ap
19	68.4	0.8	12849	US-09-902-540-963	Sequence 963, App
20	68.4	0.8	47981	US-09-679-279-1	Sequence 1, Appl
21	68.2	0.8	2277	US-08-676-974-5	Sequence 5, Appl
22	68.2	0.8	2277	US-09-098-487-5	Sequence 5, Appl
23	68.2	0.8	1260	US-09-902-540-8673	Sequence 8673, Ap
24	67	0.8	1260	US-09-902-540-918	Sequence 918, App
C 25	66.6	0.8	9191	US-08-793-273C-1	Sequence 1, Appl
26	66.6	0.8	7286	PCT-US95-11684-1	Sequence 1, Appl
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28	65.6	0.8	1104	US-09-902-540-9182	Sequence 9182, Ap
29	65.6	0.8	1836	US-09-266-965-52	Sequence 52, Appl
30	65.6	0.8	53500	US-09-266-965-52	Sequence 76, Appl
C 31	65.4	0.8	2862	US-09-252-991A-10659	Sequence 10659, A
32	65.4	0.8	2910	US-09-252-991A-10414	Sequence 10414, A
33	65.4	0.8	3111	US-09-252-991A-10504	Sequence 10504, A
C 34	64.8	0.7	601	US-09-949-016-121670	Sequence 121670, A
35	64.6	0.7	1158	US-09-902-540-3017	Sequence 3017, Ap
36	64.6	0.7	3733	US-09-902-540-639	Sequence 639, App
C 37	64.4	0.7	601	US-09-949-016-121669	Sequence 121669, A
38	63.8	0.7	50341	US-08-247-901C-1	Sequence 1, Appl
39	63.8	0.7	50341	US-09-075-904-1	Sequence 1, Appl
40	63.8	0.7	52297	US-09-426-436-1	Sequence 1, Appl
41	63.8	0.7	52297	US-08-705-557-1	Sequence 1, Appl
42	63.6	0.7	2061	US-09-252-991A-1544	Sequence 1544, Ap
43	63.6	0.7	4319	US-09-475-515-6	Sequence 6, Appl
44	63.6	0.7	41170	US-09-902-540-1267	Sequence 1267, Ap
45	62.8	0.7	4403765	US-09-103-840A-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-09-976-594-407/C
Sequence 407, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
TITLE OR INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 407
LENGTH: 2007
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 474200.1
US-09-976-594-407

Query Match      8.2%  Score 709.4;  DB 4;  Length 2007;
Best Local Similarity 99.6%  Pred. No. 6.5e-175;
Matches 732;  Conservative 0;  Mismatches 1;  Indels 2;  Gaps 2;
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QY	7913	GGGCGCCAGAGCGCTGAGAGACGGCATCAACGTGACGTGTGCGACATCCACACGGGTG	7972
DB	2007	GGGCGCCAGAGCGCTGAGAGACGGCATCAACGTGACGTGTGCGACATCCACACGGGTG	1948
QY	7973	TGAACGCGACAGCGCGAGGTTGCGGACGTGAGATGCAAGTTGCGCGCTGCGCTG	8031
DB	1947	TGAATCGGACAGAGCGCGAGGTTGCGGACGTGAGATGCAAGTTGCGCGCTGCGCTG	1888
QY	8032	CACGTGCGCTACGCGCATGATCCCTTGAGAG-AGGAGAAAGCGCGCATCTCTGAGAGGGCGG	8090
DB	1887	CACGTGCGCTACGCGCATGATCCCTTGAGAGAGAAAGCGCGCATCTCTGAGAGGGCGG	1828
QY	8091	GCAAGCGCGCTGCGCGCGCGCTGAGCGCGCGAGCAGCAGCGCTGCGCGAGAG	8150
DB	1827	GCAAGCGCGCTGCGCGCGCGCTGAGCGCGCGAGCAGCAGCGCTGCGCGAGAG	1768
QY	8151	GGGCGCGCGCTGAGAGCGAGGCGGAGAGCGGACGCTGAGCGCGCGAGAGGTGCA	8210
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QY	8211	GGGCTACGAGCGGTACTGACTCTCTGTGTGAGACGACTACCCGAGCTGCGCGAGCGC	8270

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OM nucleic - nucleic search, using sw model

Run on: September 26, 2005, 18:17:29 ; Search time 2727 Seconds
(without alignments)
18766.470 Million cell updates/sec

Title: US-10-038-854-37

Perfect score: 8645
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseq19908.*
3: Geneseq20008.*
4: Geneseq20018.*
5: Geneseq20028.*
6: Geneseq20038.*
7: Geneseq20048.*
8: Geneseq20058.*
9: Geneseq20068.*
10: Geneseq20078.*
11: Geneseq20088.*
12: Geneseq20098.*
13: Geneseq20108.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	8615	99.7	8657	12	ADH41990 Novel hum
5	8615	99.7	8657	12	ADH41992 Novel hum
6	8615	99.7	8657	12	ADH41994 Novel hum
7	8615	99.7	8657	12	ADH41996 Novel hum
8	8613.8	99.6	8675	6	ABQ82343 Human NOV
9	8594	99.4	8636	12	ADH41998 Novel hum
10	8163.6	94.4	8204	12	ADH41972 Novel hum
11	8000.6	92.5	8473	12	ADH41948 Novel hum
12	7997.8	92.5	8473	6	ABQ82345 Human NOV
13	7895.8	91.3	8487	12	ADH41976 Novel hum
14	7893.6	91.3	8487	6	ABQ82346 Human NOV
15	6789.2	78.5	8964	12	ADH01384 Teneurin
16	5952.8	68.9	6810	12	ADQ25481 Human sof
17	5305.8	61.4	5309	12	ADQ21673 Human sof
18	3714.8	43.0	8575	6	AD116607 Human NOV
19	3714.8	43.0	8575	12	ADH71271 Human gen
20	3614	41.8	3614	4	AAH14183 Human CDN

21	3614	41.8	3614	13	ADR25882	Ad25882 Breast ca
22	3589.8	41.5	8438	6	ABN95378	ABN95378 Human NOV
23	3572.8	41.3	9852	12	ADH71219	Adh71219 Human gen
24	3545.6	41.0	8797	12	ADJ75919	Adj75919 Marker ge
25	3502.2	40.5	8354	6	AB552100	AB552100 Human TEN
26	3502.2	40.5	8354	10	ADPF4829	Adf74829 Murine NO
27	3482.2	40.3	9668	12	ADH71239	Adh71239 Human gen
28	3482.2	40.3	9756	12	ADH71249	Adh71249 Human gen
29	3482.2	40.3	9823	12	ADH71257	Adh71257 Human gen
30	3482.2	40.3	9823	12	ADH71245	Adh71245 Human gen
31	3482.2	40.3	9826	5	AA514085	AA514085 Human FCT
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36	3453.8	40.0	9729	10	ADB32028	Adb32028 Human FCT
37	3453.8	40.0	9729	12	ADH71251	Adh71251 Human gen
38	3439.2	39.8	8645	6	AB578652	AB578652 Human gen
39	3423.2	39.6	8574	12	ADN42261	Adn42261 Human CDN
40	3392	39.2	6999	12	ADH71273	Adh71273 Human gen
41	3270	37.8	3270	4	AAH14671	AAH14671 Human CDN
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ALIGNMENTS

RESULT 1	ADH41968	standard; DNA; 8645 BP.
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AC	ADH41968	
DT	25-MAR-2004	(first entry)
XX	Novel human nucleic acid NOV408.	
DE	Novel human nucleic acid NOV408.	
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XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WC02003102159-A2.	
PN	11-DEC-2003.	
PD	11-DEC-2003.	
XX	04-JUN-2003; 2003WO-US017573.	
PF	04-JUN-2002; 2002US-0385490P.	
XX	04-JUN-2002; 2002US-0385615P.	
PR	04-JUN-2002; 2002US-0385755P.	
PR	05-JUN-2002; 2002US-0386041P.	
PR	06-JUN-2002; 2002US-0386355P.	
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OM nucleic - nucleic search, using bw model

Run on: September 26, 2005, 20:16:30 ; Search time 23777 Seconds
(without alignments)
17617.670 Million cell updates/sec

Title: US-10-038-854-37

Perfect score: 8645
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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	7895.8	91.3	8487	6	AX662359 Sequence
5	6789.2	78.5	8964	6	AX952856 Sequence
6	6789.2	78.5	8964	10	AB025412
7	6270	72.5	6751	6	CQ716754
8	5749.4	66.5	7816	10	AF195418
9	5305.8	61.4	5309	9	AB040888
10	4561.4	52.8	5804	10	AK122513
11	4273.8	49.4	8816	5	AB026978
12	3714.8	43.0	8575	6	AX921803
13	3614	41.8	3614	6	BD156175
14	3614	41.8	3614	6	AX876525
15	3589.8	41.5	8438	9	AX001336
16	3589.8	41.5	8438	6	AX675551
17	3566.6	41.3	8409	5	GGA279031
18	3566.6	41.3	8409	6	AX250068
19	3545.6	41.0	8797	6	CQ777485

20	3545.6	41.0	8797	6	AX250063
21	3545.6	41.0	8797	6	AX250066
22	3545.6	41.0	8797	10	AB025411
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25	3502.2	40.5	8354	6	AX556500
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27	3453.8	40.0	9729	6	AX250013
28	3451.6	39.9	8585	10	AB025413
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36	3158	36.5	7781	9	AB032953
37	3066.4	35.5	9264	5	AB026980
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ALIGNMENTS

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ACCESSION	AX662355.1	GI:29163217			
VERSION	AX662355.1				
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE					
AUTHORS	1				
	Spytek, K.A., Li, L., Wolenc, A.R., Vernet, C.A., Eisen, A., Liu, X.,				
	Malpankar, U., Shinkov, R.A., Tcherny, V.T., Spaderna, S.K.,				
	Gorman, L., Kerkuta, R., Patrajan, M., Gusev, V., Gangoli, B.A.,				
	Guo, X., Shenoy, S., Rastelli, L., Casman, S.J., Boldog, F.,				
	Burgess, C.B., Edinger, S., Eilerman, K., Gunther, B., Smithson, G.,				
	Millet, I. and Nucleic acids encoding same				
	Protein: WO 02062999-A 37 15-AUG-2002;				
	Curagen Corporation (US)				
TITLE					
JOURNAL					
FEATURES					
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	/organism="Homo sapiens"				
	/mol_type="unassigned DNA"				
	/db_xref="taxon:9606"				
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Matches 8645; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
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DB	1	TTTGGCTTCGGGCGCAAGTTCGGCAAGGGGCTTCGAGCTTGGAGGAGAGCTTGAAGT	60		
QY	61	AAGGATTAACCTTAAGAGAGGCGCAATGAGCTTGAACCTTGAAGCTTGTTCACACAGA	120		
DB	61	AAGGATTAACCTTAAGAGAGGCGCAATGAGCTTGAACCTTGAAGCTTGTTCACACAGA	120		
QY	121	GCAGTGTGTGACACAGAGAGAGAGTATGATGTGAGAGAGAGAGAGAGAGAGAGAGAG	180		
DB	121	GCAGTGTGTGACACAGAGAGAGAGTATGATGTGAGAGAGAGAGAGAGAGAGAGAGAG	180		